

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 05:30:50 : Search time 50.2472 Seconds
(without alignments)
1057.973 Million cell updates/sec

Title: US-09-698-781-3

Perfect score: 1436
Sequence: 1 MKQILPALETMTLFPVL.....KKQLVDSCKASCNSNIT 258

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

1: sp.archaea:*

2: sp.bacteria:*

3: sp.fungi:*

4: sp.human:*

5: sp.invertebrate:*

6: sp.mammal:*

7: sp.minc:*

8: sp.organelle:*

9: sp.phage:*

10: sp.plant:*

11: sp_rodent:*

12: sp.virus:*

13: sp.vertebrate:*

14: sp.unclassified:*

15: sp.virus:*

16: sp.bacteriap:*

17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1127	78.5	203	09H108	09H108 homo sapien
2	852	59.3	243	088205	088205 ratius norv
3	849	59.1	243	09R114	09R114 ratius norv
4	754.5	52.5	244	091X13	091X13 mus musculu
5	684	47.6	165	077720	077720 equus cabal
6	590.5	41.1	151	09N032	09N032 bos taurus
7	574.5	40.0	250	09D259	09D259 mus musculu
8	542.5	37.8	249	09XSD3	09XSD3 macaca mula
9	525	36.6	217	077719	077719 equus cabal
10	520	36.2	181	08UW11	08UW11 lapemis bar
11	512.5	35.7	199	08UW25	08UW25 lapemis bar
12	463	33.2	111	09N031	09N031 bos taurus
13	440	30.6	158	09R0V8	09R0V8 ratius norv
14	373.5	26.0	178	096SFE	096SFE homo sapien
15	358	24.9	153	09OXES	09OXES xenopus lae
16	345	24.0	79	077818	077818 sus scrofa

17	344	24.0	255	11	09CGM1	09CGM1 mus musculu
18	328	22.8	266	4	0969K2	0969K2 homo sapien
19	311.5	21.7	489	11	09J356	09J356 mus musculu
20	311.5	21.7	489	11	09ET66	09ET66 mus musculu
21	308.5	21.5	236	11	09DAG6	09DAG6 mus musculu
22	305.5	21.3	233	4	096L06	096L06 homo sapien
23	295.5	20.6	371	4	096K61	096K61 homo sapien
24	295.5	20.6	497	4	09H0B8	09H0B8 homo sapien
25	292	20.3	258	11	099MM7	099MM7 mus musculu
26	291	20.3	415	4	08TCB8	08TCB8 homo sapien
27	290	20.2	258	4	043692	043692 homo sapien
28	288.5	20.1	380	5	09VRY2	09VRY2 drosophila
29	288.5	20.1	392	5	0860R5	0860R5 drosophila
30	286.5	20.1	500	4	09H336	09H336 homo sapien
31	286	19.9	258	13	098ST6	098ST6 gallus galli
32	285.5	19.9	523	13	096ST5	096ST5 gallus galli
33	280.5	19.5	434	11	09D2R3	09D2R3 mus musculu
34	279.5	19.5	507	11	099MM6	099MM6 mus musculu
35	278	19.4	188	11	09Z0U6	09Z0U6 ratius norv
36	277	19.3	424	5	09X241	09X241 necator ame
37	277	19.3	424	5	09X241	09X241 ancylostoma
38	274.5	19.1	100	11	09D2T2	09D2T2 mus musculu
39	263	18.3	425	5	077153	077153 ancylostoma
40	258.5	18.0	332	11	09C035	09C035 mus musculu
41	256.5	17.9	301	5	095QF6	095QF6 caenorhabd1
42	255	17.8	253	4	09H3Y0	09H3Y0 homo sapien
43	252.5	17.6	207	5	020603	020603 caenorhabd1
44	249	17.3	208	5	09N5N3	09N5N3 caenorhabd1
45	248.5	17.3	415	5	044228	044228 halocynthia

ALIGNMENTS

RESULT 1	09H108	PRELIMINARY;	PRT;	203 AA.
ID	09H108			
AC	09H108;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	DJ417120.1 (Cysteine-rich secretory protein 3 (Crisp-3, SGP28))			
DE	(Fragment).			
GN	DJ417120.1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Phillimore B.;			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL121974; CAC19654.1; .			
DR	HSSP; P04284; ICFE.			
DR	InterPro; IPR001283; Allrgn_V5/TpX1.			
DR	Pfam; PF00188; SCP; 1.			
DR	PRINTS; PR00837; V5TPXLIKE.			
DR	ProDom; PD000542; Allrgn_V5/TpX1; 1.			
DR	SMART; SM00198; SCP; 1.			
DR	PROSITE; PS01009; SCP_AGS_PRI_SCT_1; 1.			
DR	PROSITE; PS01010; SCP_AGS_PRI_SCT_2; 1.			
FT	NON_TER 203			
FT	SEQUENCE 203 AA; 22912 MW; F80D707EED081A2B CRC64;			
Query Match	78.5%; Score 1127; DB 4; Length 203;			
Best local similarity	99.5%; Pred. No. 1.8e-101;			
Matches 202; Conservative	99.5%; 0; Mismatches 1; Indels 0; Gaps 0;			
OY	14 MKLFPVLFPVLAALPSFPAEDKDPATLTLTTOVQVRETVNKHETRAVSPARAK 73			
DB	1 MKLFPVLFPVLAALPSFPAEDKDPATLTLTTOVQVRETVNKHETRAVSPARAK 60			
OY	74 LKMEKNEAANAOKWANCNRRHSNPKDRMTSLKCGENLYWSSAPSSWSOAQISWFEY 133			

```

Db 61 LKEMNKKAANAKMANOCNRYHNSPKDRMTSLKCGENLYMSASSSSQAIOSWPEDEY 120
QY 134 NDFDGVGPKPTNAVGHYQYVWYSSYLVCGNAYCPNOKVLYKYVQCYCPAGNMANR 193
Db 121 NDFDGVGPKPTNAVGHYQYVWYSSYLVCGNAYCPNOKVLYKYVQCYCPAGNMANR 180
QY 194 LVYPEOGAPCASPDCPDGDLIC 216
Db 181 LVYPEOGAPCASPDCPDGDLIC 203

RESULT 2
088205 PRELIMINARY; PRT; 243 AA.
ID 088205;
AC 088205;
RT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Testis specific protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DONRYU; TISSUE=TESTIS;
RX MEDLINE=98340864; PubMed=9675100;
RA Maeda T., Sakashita M., Ohba Y., Nakashima Y.;
RT "Molecular cloning of the rat Tpx-1 responsible for the interaction
RT between spermatogenic and sertoli cells."
RL Biochem. Biophys. Res. Commun. 248:140-146(1998).
DR EMBL: AB009562; BAA32029.1; -.
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP: 1.
DR PROSITE: PS01009; SCP_AGS_PRL-SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL-SC7_2; 1.
SQ SEQUENCE 243 AA; 27344 MW; 2789240EA077C81 CRC64;

Query Match 59.38; Score 852; DB 11; Length 243;
Best Local Similarity 61.04; Pred. No. 1.1e-74;
Matches 151; Conservative 31; Mismatches 61; Indels 2; Gaps 2;

QY 14 MTLFVLLFLVAGLLPSFPANEDKDPATLTTOTQVOREIYVKNHLELRAVSPPARNM 73
Db 1 MAMFOVMLFVAVLLP-LPTEGKDPFATLTITNOIOVOREIITAKHNEIRQVSPGSI 59
QY 74 LKEMNKKAANAKMANOCNRYHNSPKDRMTSLKCGENLYMSASSSSQAIOSWPEDEY 133
Db 60 LKEMNKKAANAKMANOCNRYHNSPKDRMTSLKCGENLYMSASSSSQAIOSWPEDEY 119
QY 134 NDFDGVGPKPTNAVGHYQYVWYSSYLVCGNAYCPNOKVLYKYVQCYCPAGNMANR 193
Db 120 ENFVGVGAK-PNSAVGHYQYVWYSSYLVCGNAYCPNOKVLYKYVQCYCPAGNMANR 178
QY 194 LVYPEOGAPCASPDCPDGDLICNCKYEDLYSNCKSLKLTTCRQHLVDRSCASCNC 253
Db 179 KSTPYHOGTGPCASPCPNCDNGLCTNCSDFEDLLSNCKSLKSGCKHLLKAKCEATCIC 238
QY 254 SNSIY 258
Db 239 EDKIH 243

RESULT 3
09RIL4 PRELIMINARY; PRT; 243 AA.
ID 09RIL4;
AC 09RIL4;
RT 01-MAY-2000 (TREMBLrel. 13, Created)

```

```

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DT Cysteine-rich secretory protein-2 clisp-2.
GN Tpx-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=98284327; PubMed=9621307;
RA O'Bryan M.K., Loveland K.L., Herzfeld D., McFarlane J.R., Hearn M.T.,
RA de Kretser D.M.;
RT "Identification of a rat testis-specific gene encoding a potential rat
RT outer dense fibre protein."
RL Mol. Reprod. Dev. 50:313-322(1998).
DR EMBL: AF078552; ABA48090.1; -.
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP: 1.
DR PROSITE: PS01009; SCP_AGS_PRL-SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL-SC7_2; 1.
SQ SEQUENCE 243 AA; 27429 MW; FA604ECES0F7D3BA CRC64;

Query Match 59.18; Score 849; DB 11; Length 243;
Best Local Similarity 61.24; Pred. No. 2.2e-74;
Matches 150; Conservative 31; Mismatches 62; Indels 2; Gaps 2;

QY 14 MTLFVLLFLVAGLLPSFPANEDKDPATLTTOTQVOREIYVKNHLELRAVSPPARNM 73
Db 1 MAMFOVMLFVAVLLP-LPTEGKDPFATLTITNOIOVOREIITAKHNEIRQVSPGSI 59
QY 74 LKEMNKKAANAKMANOCNRYHNSPKDRMTSLKCGENLYMSASSSSQAIOSWPEDEY 133
Db 60 LKEMNKKAANAKMANOCNRYHNSPKDRMTSLKCGENLYMSASSSSQAIOSWPEDEY 119
QY 134 NDFDGVGPKPTNAVGHYQYVWYSSYLVCGNAYCPNOKVLYKYVQCYCPAGNMANR 193
Db 120 ENFVGVGAK-PNSAVGHYQYVWYSSYLVCGNAYCPNOKVLYKYVQCYCPAGNMANR 178
QY 194 LVYPEOGAPCASPDCPDGDLICNCKYEDLYSNCKSLKLTTCRQHLVDRSCASCNC 253
Db 179 KSTPYHOGTGPCASPCPNCDNGLCTNCSDFEDLLSNCKSLKSGCKHLLKAKCEATCIC 238
QY 254 SNSIY 258
Db 239 EDKIH 243

RESULT 4
09IXA3 PRELIMINARY; PRT; 244 AA.
ID 09IXA3;
AC 09IXA3;
RT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to acidic epididymal glycoprotein 1.
GN Aeg1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPERMATIDY;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC011150; AAH1150.1; -.
DR MGD; MGI:102553; Aeg1.

```

DR InterPro: IPR001283; Allrgn_V5/Tpx1.

DR Pfam: PF000342; Allrgn_V5/Tpx1; 1.
DR PRODOM: PD000542; SCP_Ag5_Pri_Sc7_1; UNKNOWN_1.
DR PROSITE: PS01009; SCP_Ag5_Pri_Sc7_1; UNKNOWN_1.
DR PROSITE: PS01010; SCP_Ag5_Pri_Sc7_2; UNKNOWN_1.
SO SEQUENCE 244 AA; 27622 MW; BDE122E2E5E8146 CRC64;

Query Match 52.5%; Score 754.5; DB 11; Length 244;
Best Local Similarity 54.3%; Pred. No. 3.3e-65;
Matches 133; Conservative 39; Mismatches 72; Indels 1; Gaps 1;

OY 14 MTLFPLFLVAGLLPSPFANEDKDPATALLTQTOVOREIYKHNELRRVSPRANM 73
DB 1 MALMLVFLAVALPPLSLDSSQENRLEKLTITMSPEEITSKHNLRRVSSGDL 60
OY 74 LKMKNEKKAANAKNANOCNRYNSPKDRMTSLKCGENLYSSAPSSQAIOSEFDEY 133
DB 61 LKMKNYDAQVNAQOMADKCTFHSPIELRTNLMCGENSPSSYLAWSAIOGVNEY 120
OY 134 NDFEGVGPKTPNNAVGHYTOVWYSSYLVCGNAYCPNOKVLYKYYVQCPAGNMANR 193
DB 121 KDLTYDVGPKDPDVGHYTOVWYSSYLVGCNAYCPNOKVLYKYYVQCPAGNMANR 179
OY 194 LVPYRQAGAPCASPNDGGLCTNCKGKEDLYSNCKSLKTLTKHOLVRSKASGNC 253
DB 180 LVPYRQAGAPCASPNDGGLCTNCKGKEDLYSNCKSLKTLTKHOLVRSKASGNC 239
OY 254 SNSIY 258
DB 240 EGRKH 244

RESULT 5
077720 PRELIMINARY; PRT: 165 AA.
ID 077720;
AC 077720;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cysteine-rich secretory protein-2 (Fragment).
GN Crisp-2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA Schambooy A., Toepfer-Petersen E.;
RU Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ006632; CAA07160.1;
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01010; SCP_Ag5_Pri_Sc7_2; 1.
FT NON-TER 1
FT NON-TER 165
SO SEQUENCE 165 AA; 18402 MW; 91172E8A7D4680B9 CRC64;

Query Match 47.6%; Score 684; DB 6; Length 165;
Best Local Similarity 69.7%; Pred. No. 1.4e-58;
Matches 115; Conservative 18; Mismatches 32; Indels 0; Gaps 0;
OY 69 PARNMLKMKNEKKAANAKNANOCNRYNSPKDRMTSLKCGENLYSSAPSSQAIOSEFDEY 128
DB 1 PARNMLKMKNEKKAANAKNANOCNRYNSPKDRMTSLKCGENLYSSAPSSQAIOSEFDEY 60
OY 129 WFDYNDVDFGVGPKTPNNAVGHYTOVWYSSYLVCGNAYCPNOKVLYKYYVQCPAGN 188
DB 61 WFDYNDVDFGVGPKTPNNAVGHYTOVWYSSYLVCGNAYCPNOKVLYKYYVQCPAGN 120

OY 169 NMANRLVPEYEGAPCASPNDGGLCTNCKGKEDLYSNCKSLK 233
DB 121 NMANRLVPEYEGAPCASPNDGGLCTNCKGKEDLYSNCKSLK 165

RESULT 6
09N0J2 PRELIMINARY; PRT: 151 AA.
ID 09N0J2;
AC 09N0J2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cysteine-rich secretory protein-2 (Fragment).
GN Crisp-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA Gentzel M., Schambooy A., Toepfer-Petersen E.;
RU Identification of Crisp proteins of stallion and bull.
RU Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ277708; CAB90614.1; Allrgn_V5/Tpx1.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP; 1.
FT NON-TER 151
FT NON-TER 151
SO SEQUENCE 151 AA; 16703 MW; DAZFLAE62929E1 CRC64;

Query Match 41.1%; Score 590.5; DB 6; Length 151;
Best Local Similarity 71.7%; Pred. No. 1.5e-49;
Matches 109; Conservative 16; Mismatches 26; Indels 1; Gaps 1;
OY 14 MTLFPLFLVAGLLPSPFANEDKDPATALLTQTOVOREIYKHNELRRVSPRANM 73
DB 1 MALMLVFLAVALPPLSLDSSQENRLEKLTITMSPEEITSKHNLRRVSSGDL 59
OY 74 LKMKNEKKAANAKNANOCNRYNSPKDRMTSLKCGENLYSSAPSSQAIOSEFDEY 133
DB 60 LKMKNYDAQVNAQOMADKCTFHSPIELRTNLMCGENSPSSYLAWSAIOGVNEY 119
OY 134 NDFEGVGPKTPNNAVGHYTOVWYSSYLVCGNAYCPNOKVLYKYYVQCPAGNMANR 165
DB 120 LDFYGVGPKSAGSVGHYTOVWYSSYLVGCNAYCPNOKVLYKYYVQCPAGN 151

RESULT 7
09D259 PRELIMINARY; PRT: 250 AA.
ID 09D259;
AC 09D259;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 9230112K08R1K protein.
GN 9230112K08R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EPIDIDYMIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Krenn P., Lewis S., Matsuo T., Nakado I., Pesole G., Quackenbush J.,
 RA Schram L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boiteill D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa T., Kawaji H., Kontsuki S.,
 RA Hayashizaki Y.,
 RA Functional annotation of a full-length mouse cDNA collection.*;
 RL Nature 409:685-690(2001).
 DR EMBL: AK020340; BAB32077.1;
 DR MGD: MGI:1925331; 9230112K08R1K.
 DR InterPro: IPR001283; Allrgn_V5/TpX1.
 DR Pfam: PF00188; SCP: 1.
 DR PRINTS: PR00837; V5TPXLIKE.
 DR PRODOM: PD000542; Allrgn_V5/TpX1. 1.
 DR SMART: SM00198; SCP: 1.
 DR PROSITE: PS01009; SCP_AGS_PRL-SC7_1; 1.
 DR SEQUENCE 250 AA; 28704 MW; 747845FF2FEDB9D1 CRC64;
 SO
 Query Match 40.0%; Score 574.5; DB 11; Length 250;
 Best Local Similarity 46.1%; Pred. No. 1e-47;
 Matches 113; Conservative 35; Mismatches 90; Indels 7; Gaps 5;
 OY 19 VLLFLVAGLILPSF---PANEDKDPATLALT-TOTVOGREIVNKHNLRAVSPARNML 74
 DB 6 ILLLVAAFPVVTIRPLKDR-ALXNKLTIESOTEOEIVVTHNAFRKYSPPARNML 64
 OY 75 KHEHKEAANAOKNACNVRHSNPKD-RMTSLKCGENLYSSAPSSQSIQSPFDEY 133
 DB 65 KVSMSAAAEARILARYCKSDSDLEHRLPNFCEGNLMHRYSSSKYIEIWFNES 124
 OY 134 NDFEGVGPRTPNV-VGHYTOVWYSSYLVCGNAYCPNQKYLKLYYVCOYCPAGNMAN 192
 DB 125 KYFKYGEWPSITDDIETDHTQWMASTYLVCDAVACRQKATATLYVCHYCHGCHGNQD 184
 OY 193 RLYVYFEGAPCASPNCDDGLCTNGCKYEDLYSNCKSLKLTCTCKHOLVDSCKASCN 252
 DB 185 TLNMFYKSGSPDCDPCPNCGDGLCTNPCTIYDEYVNCNDYVKLYGCSHNAVQPCCKASCL 244
 OY 253 CNSI 257
 DB 245 CTTEI 249
 RESULT 8
 OYXSD3 PRELIMINARY; PRT; 249 AA.
 AC OYXSD3;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI-TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sivasubramanian P., Richardson R.T., Hall S., Hamil K.G., French F.S.,
 RA O'Rand M.G.;
 RT Cloning and characterization of an androgen dependent acidic
 RT epididymal glycoprotein/crispl-like protein from the monkey.*;
 RL EMBL: AF13894; AAD27611.1;
 DR InterPro: IPR001283; Allrgn_V5/TpX1.

DR Pfam: PF00188; SCP: 1.
 DR PRINTS: PR00837; V5TPXLIKE.
 DR PRODOM: PD000542; Allrgn_V5/TpX1. 1.
 DR SMART: SM00198; SCP: 1.
 DR PROSITE: PS01010; SCP_AGS_PRL-SC7_2; 1.
 SO SEQUENCE 249 AA; 28653 MW; 26DD3071C5F1F2A1 CRC64;
 Query Match 37.8%; Score 542.5; DB 6; Length 249;
 Best Local Similarity 44.9%; Pred. No. 1.3e-44;
 Matches 109; Conservative 34; Mismatches 95; Indels 5; Gaps 4;
 OY 20 LLLFLVAG--LLDFSP-ANEDKDPATLALTTOVOGREIVNKHNLRAVSPARNMLK 76
 DB 6 LLLFLVAACTLLPLMKRSKAKLFLNKLTYDLPNVQOEIVVTHNAFRKYSPPARNMLK 65
 OY 77 EMNEEAANAOKNACNVRHSNPKD-RMTSLKCGENLYSSAPSSQSIQSPFDEYND 135
 DB 66 SMSEEAANAOKNACNVRHSNPKD-RMTSLKCGENLYSSAPSSQSIQSPFDEYND 125
 OY 136 FDFGVGPRTPNV-VGHYTOVWYSSYLVCGNAYCPNQKYLKLYYVCOYCPAGNMAN 194
 DB 126 FRIQMPSTDDISTDRTQWMASTYLVCDAVACRQKATATLYVCHYCHGCHGNQD 185
 OY 195 VYVYEGAPCASPNCDDGLCTNGCKYEDLYSNCKSLKLTCTCKHOLVDSCKASCNS 254
 DB 186 HEYKKGVPCEACPNNCEDKLTNPCTIYDEYVDCSLFVRICGNHSTPRMCKATCLCD 245
 OY 255 NSI 257
 DB 246 TEI 248
 RESULT 9
 OY 077719 PRELIMINARY; PRT; 217 AA.
 AC 077719;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 OS Cystine-rich secretory protein-1 (Fragment).
 GN CRISP-1.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI-TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EPIDIDYMS;
 RA Schambony A., Toepfer-Petersen E.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ006631; CA07159.1;
 DR InterPro: IPR001283; Allrgn_V5/TpX1.
 DR Pfam: PF00188; SCP: 1.
 DR PRINTS: PR00837; V5TPXLIKE.
 DR PRODOM: PD000542; Allrgn_V5/TpX1. 1.
 DR SMART: SM00198; SCP: 1.
 DR PROSITE: PS01009; SCP_AGS_PRL-SC7_1; 1.
 DR PROSITE: PS01010; SCP_AGS_PRL-SC7_2; 1.
 FT NON-TER 1
 SO SEQUENCE 217 AA; 24832 MW; 86AA6778A244CAE8 CRC64;
 Query Match 36.6%; Score 525; DB 6; Length 217;
 Best Local Similarity 45.4%; Pred. No. 5.5e-43;
 Matches 98; Conservative 33; Mismatches 83; Indels 2; Gaps 2;
 OY 44 LLLTOVOGREIVNKHNLRAVSPARNMLKEMNEEAANAOKNACNVRHSNPKD- 102
 DB 1 VLDLATVOEIVVTHNAFRKYSPPARNMLKSMSEEAANAOKNACNVRHSNPKD- 60
 OY 103 RMTSLKCGENLYSSAPSSQSIQSPFDEYDFGVGPRTPN-VAVGHYTOVWYSSYL 161
 DB 61 RITFTCGANMHLTSPISMSVIGMWFSESKYFYFGWISTDEVIIEHYTQWMASTY 120

[illegible]

```

SEQUENCE FROM N.A.
RA Williams S.:
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL AL359458; CAC34981.1;
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP_1.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR PROSITE: PS01009; SCP_AGS_Prl_Sc7_1; UNKNOWN_1.
DR SEQUENCE 178 AA; 20462 MW; 18739B26BEF7E84 CRC64;
SQ
Query Match                26.0%; Score 373.5; DB 4; Length 178;
Best Local Similarity      47.1%; Pred. No. 2,2e+28;
Matches    81; Conservative 21; Mismatches   63; Indels       7; Gaps        5;

OY 20 LLEIYAG--LLP--SFRANDKDPATALLTTOYOOREVYNHNELRRASPPARMLK 75
Ddb 6 LLELYAACLPLSLMKKKKSARD-QPNKVTDLPNOVEELYHNLRLRVRYPSPAMLK 64
OY 76 MEKNKEAANAOKMANOCNRYHSNPKD-RMTSLKGCEILTYSSAPSSQAIOGSMFDENY 134
Ddb 65 MSNSEBAQNRIRISKYCDDTESNPLERLNTCGENMHMITYSPVSSVIYGWSEST 124
OY 135 DEFGEGGRTPNAV-VGHITOVVVYSYLVCAGCAAYPNOKVLKYUYCYQC 185
Ddb 125 SFKHGMFTTTDDDTIDHTYTQTVMATSYLICAIASCROGGSRPLYUOHIC 176

RESULT 15
O90XES PRELIMITARY: PRT: 153 AA.
AC O90XES:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Allurin (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
CC Xenopodidae; Xenopus.
CX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21457293; PubMed=11562501;
RA Olson J.H., Xiang X., Ziegert T., Kittelson A., Rawls A., Biebert A.L.,
RA Chandler D.E.;
RT "Allurin, a 21-kDa sperm chemoattractant from Xenopus egg jelly, is
RT related to mammalian sperm-binding proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:11205-11210(2001).
DR EMBL AF393653; AAL12003.1;
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP_1.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR PROSITE: PS01009; SCP_AGS_Prl_Sc7_1; UNKNOWN_1.
DR PROSITE: PS01010; SCP_AGS_Prl_Sc7_2; UNKNOWN_1.
CT NON TER 1
SF SEQUENCE 153 AA; 17684 MW; ED1A246785FC3C6A CRC64;
SQ
Query Match                24.9%; Score 358; DB 13; Length 153;
Best Local Similarity      46.3%; Pred. No. 5,8e+27;
Matches    69; Conservative 22; Mismatches   52; Indels       6; Gaps        3;

OY 72 NMLEKMNEKAANAKWANOCNRYHSNPKR---WTSLKGCEILTYSSAPSSQAIO 127
Ddb 1 DMKMYWCDCPALAAINAFATQCSMYSHLSIEERHIKEPIDVGCENIMYSTAKSDMSTVID 60
OY 128 SMPDEVNDPGCVOPKTPNALNVCHITGVVVSVSYLVLCAGCAAYPNOKVLKYUYCOCPA 187
Ddb 61 SWNNESDFPAVGKG-KISDKRFIGHTGYVMMAKSYLICAVNPFCKEK -YHFVCHIGPM 118
OY 188 GNANRLVYFPEDGACPCASCPRNCDGCLC 216
Ddb 119 GNADSVPRPYEBEGMCASCPESCDDKLK 147

```

Fri Mar 14 14:00:11 2003

us-09-698-781-3.rspt

Pag 7

Search completed: March 14, 2003, 05:42:59
Job time : 52.2472 secs
